ID (e.g., as3344): _____ Name: _____ Expected Course LetterGrade (+5pts): ____

BIOMED 201 - Programming & Modeling for BME

Final Exam, 2014.12.08, Instructor: Ahmet Sacan

Sign the honor code below. **No credit will be given for the exam without a signed pledge.**

I have neither given nor received aid on this examination.

Signed: _____ *Sign-out Time:* _____

There are ***7 questions*** *in this exam. Turn in your paper exam before you start working on Questions 6-7. Submit your programs for Questions 6-7 on ProgrammingBank.*

Q6 (30 pts). *Loops*. Write a function **b=wsmooth(a)** that takes a vector **a** of length $\boldsymbol{n \geq 2}$ and employs a weighted moving average smoothing and returns the resulting vector **b**. The first and last elements of **a** remain unchanged; the rest of the elements are smoothed as shown below.

$$b_1 = a_1$$
$$b_2 = \frac{a_1}{4} + \frac{a_2}{2} + \frac{a_3}{4}$$
$$b_3 = \frac{a_2}{4} + \frac{a_3}{2} + \frac{a_4}{4}$$
$$b_4 = \frac{a_1}{4} + \frac{a_2}{2} + \frac{a_3}{4}$$
$$\dots$$
$$b_{n-1} = \frac{a_{n-2}}{4} + \frac{a_{n-1}}{2} + \frac{a_n}{4}$$
$$b_n = a_n$$

```
>> disp(wsmooth([4 2 4]))
     4     3     4

>> disp(wsmooth([4 2 2 4]))
    4.0000    2.5000    2.5000    4.0000

>> disp(wsmooth(1:8))
     1     2     3     4     5     6     7     8

>> disp(wsmooth([5 5 5 5 5 5]))
     5     5     5     5     5     5
```

Q7 (20 pts). *Strings, File, Loops*. Identifying the proteins a drug binds to is useful for determining its side-effects and for finding other diseases the drug can be used for. Drugbank is a database that collects information about drugs and their target proteins. In this problem, you will write a function that uses a Drugbank text file and returns a list of proteins that a drug binds to. An example Drugbank file can be downloaded from **http://sacan.biomed.drexel.edu/ftp/bmeprog/drugbank_targets_sample.csv** The drugbank file is a comma separated file, where the first row is the header row, and each of the other rows contains information on a protein and lists the drugs it binds to. For each protein, the numerical drug ids are represented by a 7-character string with a prefix of 'DB' and separated by semicolons. Write a function **drug2ptns(drugid,file)** that takes a drug id and a drugbank file and returns all the protein ids the drug is listed to bind, as a cell array of strings. The drug id given to your function can be either a string with the 'DB' prefix, or a number.

```
>> disp(drug2ptns('DB00117','drugbank_targets_sample.csv'))
    'P19113'
>> disp(drug2ptns('DB00114','drugbank_targets_sample.csv'))
    'P19113'    'P06737'
>> disp(drug2ptns('DB00303','drugbank_targets_sample.csv'))
    'P45059'
>> disp(drug2ptns(117,'drugbank_targets_sample.csv'))
    'P19113'
```

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Q1 (10 pts). *Base conversion*. Write the decimal number **65** in **binary** and in **base-5**.

binary:	In base 5:

Q2 (10 pts). *Vectorized code*. Let **n** be an even number. Write a single statement to assign into **s** the value of the following sum. Do not use loops.

$s = 1 - 2 + 3 - 4 + \ ... + (n-1) - n$

```
s =
```

Q3 (10 pts). *structs, indexing*. Fill in the output below.

```
>> p=struct('a',{3 5 7 11 13 17},'b',{19 23 29 31 37 41});
>> disp( [p( mod([p.a],5)==2).b ] )
```

_____

Q4 (10 pts). *cells*. Fill in the output below.

```
>> m={ [1 5] {1 10}; 1:20 {1:30}};
>> disp([numel(m(1:3)) numel(m{1}) numel(m{2}) numel(m{end}) numel(m{end}{1})])
```

_____

Q5 (10 pts). *cells, indexing*. Fill in the output below.

```
>> s='mouse';
>> dict={'human',3; 'mouse',7; 'fruitfly',11};
>> I=strcmp(dict(:,1),s);
>> dict{I,2} = dict{I,2} +1;
>> disp([ dict{:,2} ]);
```

_____